



Connecting and merging fibres: Pathway extraction by combining probability maps [☆]

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ABSTRACT

Probability mapping of connectivity is a powerful tool to determine the fibre structure of white matter in the brain. Probability maps are related to the degree of connectivity to a chosen seed area. In many applications, however, it is necessary to isolate a fibre bundle that connects two areas. A frequently suggested solution is to select curves, which pass only through two or more areas. This is very inefficient, especially for long-distance pathways and small areas. In this paper, a novel probability-based method is presented that is capable of extracting neuronal pathways defined by two seed points. A Monte Carlo simulation based tracking method, similar to the Probabilistic Index of Connectivity (PiCo) approach, was extended to preserve the directional information of the main fibre bundles passing a voxel. By combining two of these extended visiting maps arising from different seed points, two independent parameters are determined for each voxel: the first quantifies the uncertainty that a voxel is connected to both seed points; the second represents the directional information and estimates the proportion of fibres running in the direction of the other seed point (connecting fibre) or face a third area (merging fibre). Both parameters are used to calculate the probability that a voxel is part of the bundle connecting both seed points. The performance and limitations of this DTI-based method are demonstrated using simulations as well as *in vivo* measurements.

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Introduction

Diffusion-weighted MRI (Le Bihan, 1995) enables the determination of the neuronal fibre direction (Basser et al., 1994; Kreher et al., 2005; Moseley et al., 1990; Tuch et al., 2002) or of the fibre orientation density function (Jansons and Alexander, 2003; Liu et al., 2004; Tournier et al., 2004; Tuch et al., 2003; Wedeen et al., 2005). It allows the non-invasive reconstruction of neuronal pathways in white matter. Over the last few years, several fibre tracking algorithms have been developed and applied to neuroscientific as well as clinical applications (Johansen-Berg and Behrens, 2006).

There are two major classes of fibre tracking approaches available: the walker approaches are based on tracing trajectories through the volume. The local traversing direction is derived from the local diffusion distribution either deterministic (Basser et al., 2000; Mori et al., 1999) or probabilistic

(Behrens et al., 2003; Koch et al., 2002; Lazar and Alexander, 2005; Parker et al., 2003). For the probabilistic methods, random curves are generated repeatedly according to a Monte Carlo simulation to determine the degree of connectivity of a voxel to the seed region. This is estimated by the frequency such random walk passed through the voxel. The other class is derived from the Hamilton–Jacobi formalism. Instead of propagating many independent walkers through the volume, a front is evolved depending on the tensor field (Parker et al., 2002). The speed, the front is evolving through the volume is defined by the diffusion tensor. The time, the front needs to arrive at a certain point is used to specify the connectivity to the seed point.

These methods consider all connections in the brain, which originate at a specified seed point. However, of central interest are neuronal pathways connecting two functional areas, e.g. long-distance association tracks connecting temporal and frontal areas in the language system (Catani et al., 2005) or parietal and frontal areas in the attention system (Bartolomeo et al., 2007). To extract such specific point to point pathways with methods of the walker class, several authors suggested the selection of a fascicle by placing

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